

### REMARKS

Claims 46 and 50-56 are active. Independent claim 46 has been amended to include the limitations of claim 47. Claims 48-49 presented in the Amendment filed after final rejection have not been entered. New claims 50-51 correspond to these claims which depend from claim 46 and separately claim methods based on either SEQ ID NO: 1 or 2 as previously described by claim 45. Claim 45 has been replaced by new claim 52. New claims 53-56 track limitations in claim 52 but in light of the remarks in the Advisory Action use alternative language to define the nucleic acid sequence or claimed fragments. The word “contiguous” used in claim 52 means the eight or more amino acids are adjoining and next to each other. This term doesn’t introduce a new concept since fragments of adjoining nucleotides of this length sequences are disclosed on lines 17-18 at page 10 of the specification. No new matter is believed to have been introduced.

### Restriction/Election

The Applicants previously elected with traverse **Group I**, claims 1-6, 37 and 45, directed to a method of identifying ligands or aptamers. The requirement has been made FINAL.

### Rejection—35 U.S.C. §112, first paragraph

Claims 2 and 45 were rejected under 35 U.S.C. 112, first paragraph, as lacking adequate descriptive support. This rejection is moot in view of the cancellation of these claims.

### Rejection—35 U.S.C. §112, first paragraph

Claims 1-6, 37, and 45-47 were rejected under 35 U.S.C. 112, first paragraph, as lacking adequate descriptive support. This rejection is moot in view of the cancellation of claims 1-6, 37, 45 and 47, in view of the amendment of claim 46 and in view of the Applicants prior

remarks. At the time of invention it was well within the skill of the art to select an adequate starting mixture of nucleic acids for performing an aptamer selection according to the systematic evolution of ligands by exponential enrichment (SELEX) method dating back to 1990. It should be appreciated that the starting mixture need not be enriched in particular sequences and that SEQ ID NO: 1 and 2 only relate to the primer sequences necessary to perform the RT-PCR enriching steps (see Example 1) but that other primer sequences can be used.

Rejection—35 U.S.C. §112, second paragraph

Claims 2 and 45-47 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite. This rejection is moot in view of the cancellation of claims 2, 45 and 47 and in view of the amendment of claim 46. The phrase “at least 8 contiguous nucleotides” now appearing in claim 51 refers to fragments that are subsequences of SEQ ID NO: 1 or 2 that have at least eight nucleotides of SEQ ID NO: 1 or 2 in a row.

Rejection—35 U.S.C. §103(a)

Claims 1-6, 37 and 45 were rejected under 35 U.S.C. §103(a) as being unpatentable over Chen, PNAS 10:9226 in view of Yayon, et al., U.S. Patent No. 7,498,416. This rejection is moot in view of the cancellation of these claims.

Conclusion

In view of the amendments and remarks above, the Applicants respectfully submit that this application is now in condition for allowance. An early notice to that effect is earnestly solicited.

Respectfully submitted,

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A handwritten signature in black ink, appearing to read "Thomas M. Cunningham", is written over a horizontal line.

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